

FIG. 1A

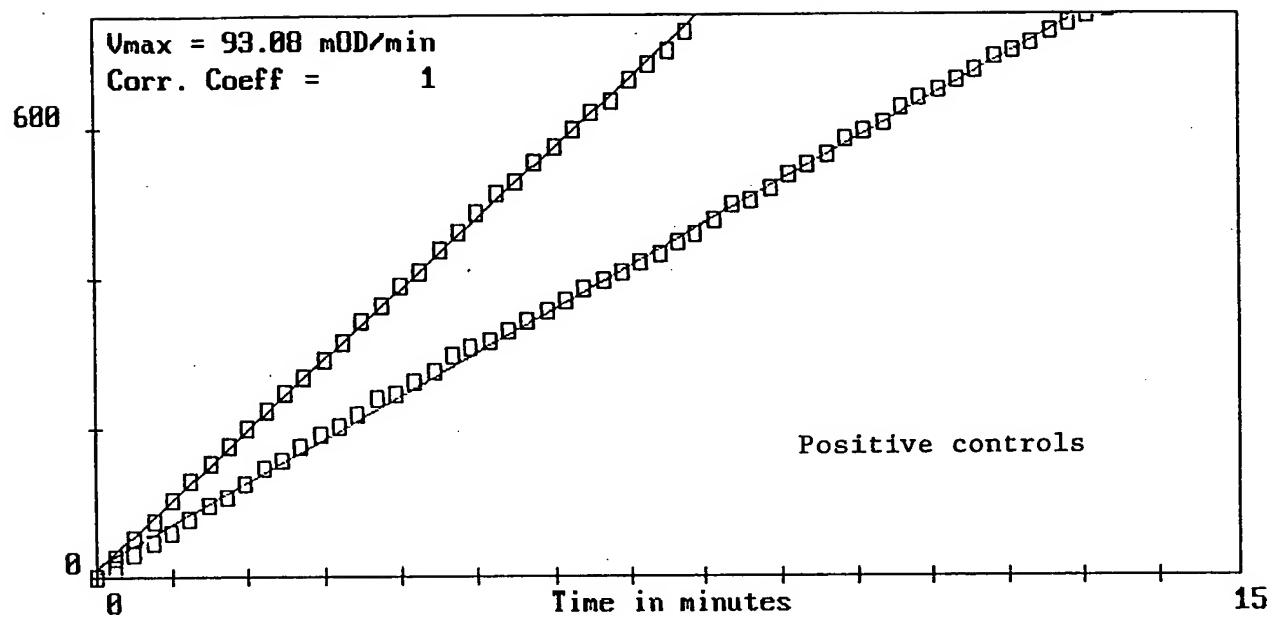


FIG. 1B

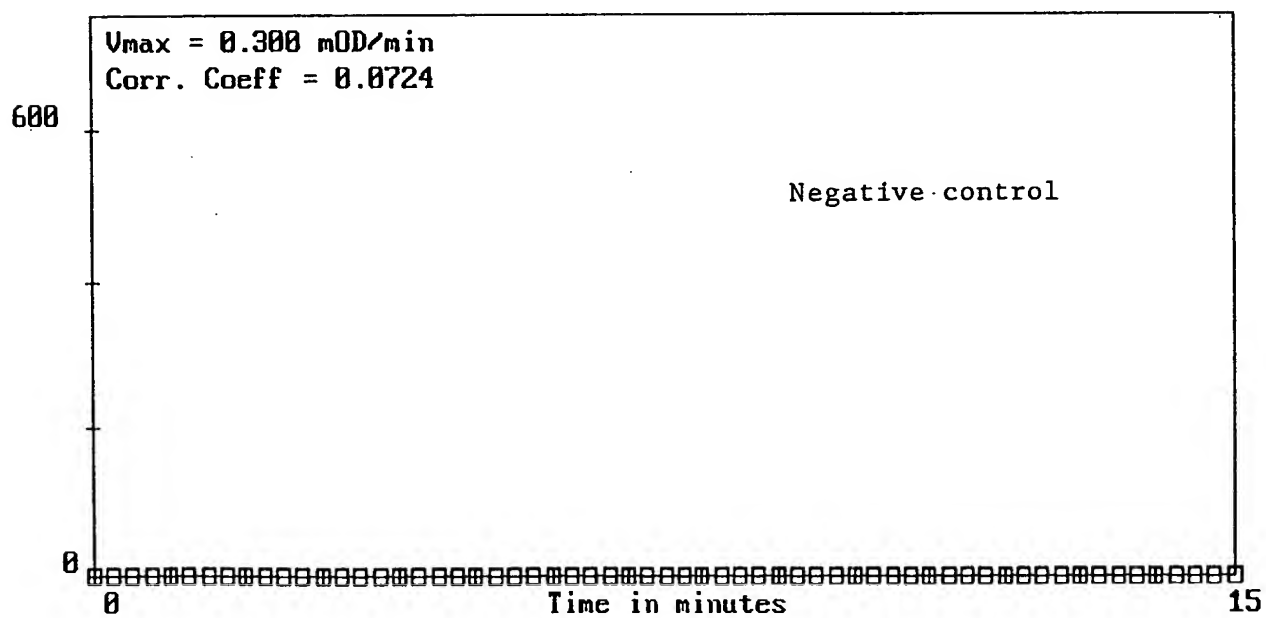


FIG. 1C

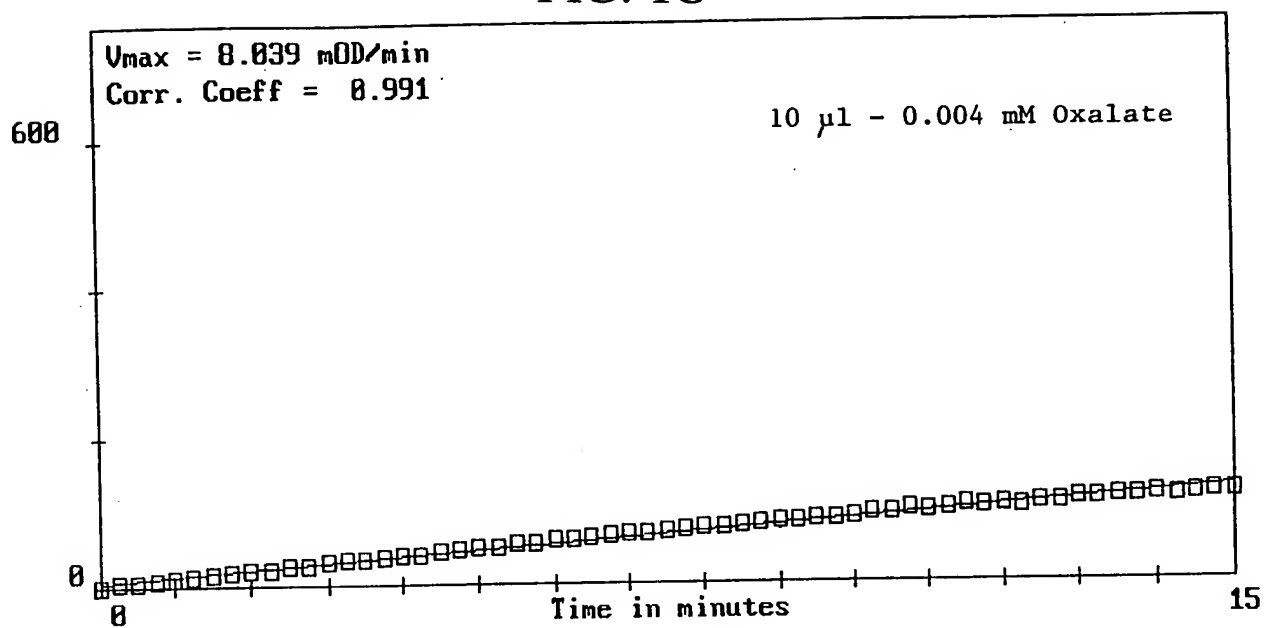


FIG. 1D

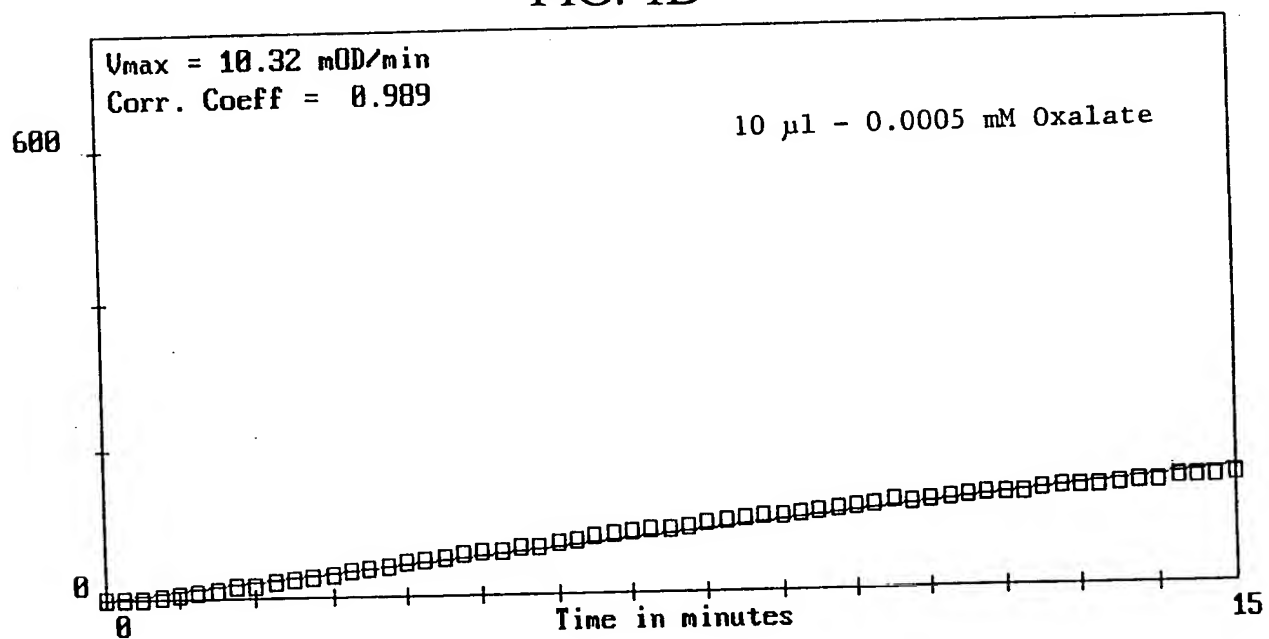


FIG. 1E

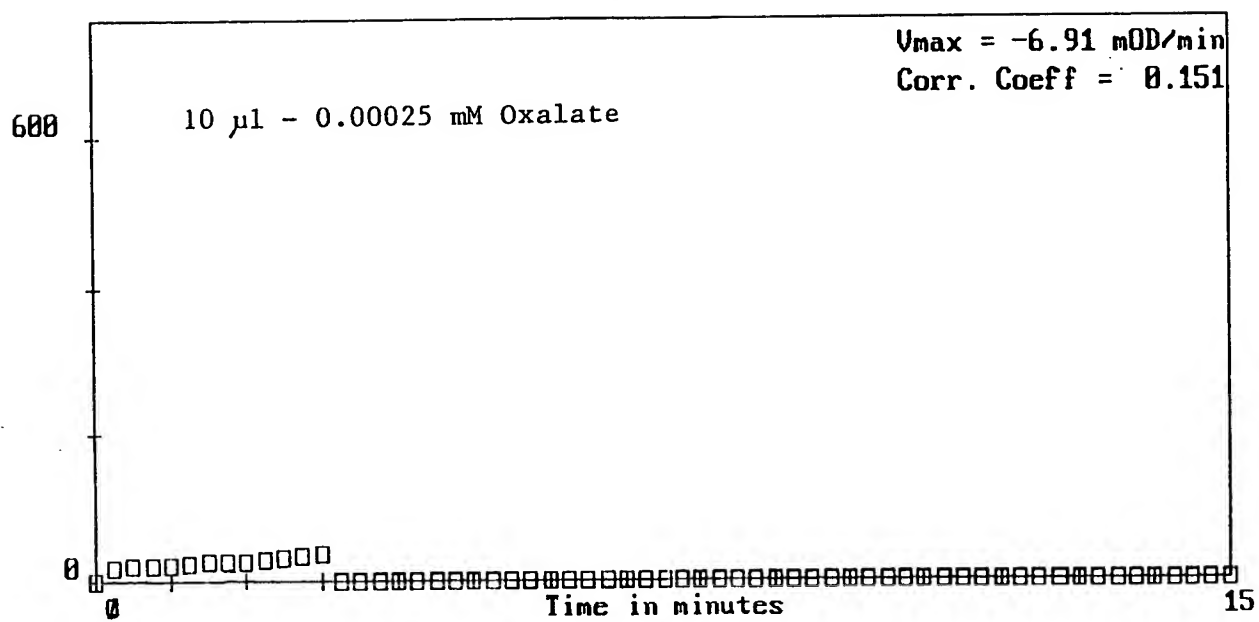


FIG. 2A

Hind III site
 -161 ||
 -109
AAGCITGGCTTCATTTTGAGATGTTATGCGAAGTGTAGCAACCCCAAGTTAGTA
 -13
 -1
 CCTTCAGCCCTTTGGCGAAGTTTTCTTTCTTGGCAGTTCCCTTCGGGGAAACAGCCACAGAGAATAAAACCAAAAGTTGTACCAACGACGAAGGAAATGAGAAATT
 -45
 -77
 1
 M T K P L D G I N V L D F T H V Q A G P A C T Q M M G F L G A N V I K I
 108
 ATGACTAAACCATTAGATGGAATTAATGCTTGACTTTACCCACGTCAGGAGGTCCTGCTGACAGATGATGGTTTCTTGGCGCAACGTCATCAAGATT
 >--5'-degen-primer->
 TRYPSIN DIGEST
 216
 E R R G S G D M T R G W L Q D K P N V D S L Y F T M F N C N K R S I E L
 GAAAGACGTGGTTCGGAGATATGACTCGTGGATGGCTGCAGGACAAACCAAAATGTTGATTCCTGTATTTTCCAGTGTTCACACTGTAAACAAACGTTTCGATTGAACCTG
 <---3'-primer---
 324
 D M K T P E G K E L L E Q M I K K A D V M V E N F G P G A L D R M G F T
 GACATGAAAACCCCGGAAGCAAGAGCTTCTGGAAACAGATGATCAAGAAAGCGACGTCATGGTCGAAAACCTTCGGACCAGGCGCACTGGACCGTATGGGCCTTACT
 -----<
 432
 W E Y I Q E L N P R V I L A S V K G Y A E G H A N E H L K V Y E N V A Q
 TGGGAATACATTTCAGGAACCTGAATCCACCGGTCATTTCTGGCTTCCGTTAAAGGCTATGCAGAAGGCCCAACCAACACCTGAAAGTTTATGAAACGTTGCACAG
 540
 C S G G A A A T T G F W D G P P T V S G A A L G D S N S G M H L M I G I
 TGTTCGGCGGTGCTGCAGCTACCAACCGGTTTCTGGGATGGTCTCTCAACCGTTTCCGGCGCTGCTCTGGGTGACTCCAACCTCCGGTATGCACCTGATGATCGGTATT
 648
 L A A L E M R H K T G R G Q K V A V A M Q D A V L N L V R I K L R D Q Q
 CTGGCCGCTCTGGAAATGCGTCACAAAACCGCGGTGGTCAGAAAAGTTGCCGTGCTATGCAGGACGCTGTTCTGAACTCGTTCGTTATCAAACTGCGTGACCAAGCAA
 756
 R L E R T G I L A E Y P Q A Q P N F A F D R D G N P L S F D N I T S V P
 CGTCTGGAAGAAGACCGGCTTCTGGCTGAATACCCACAGGCTCAGCTAAGCTTTGCCCTTCGACAGAGACGGTAACCCACTGTCTTCGACAACATCCTCCGTTCCA

FIG. 2B

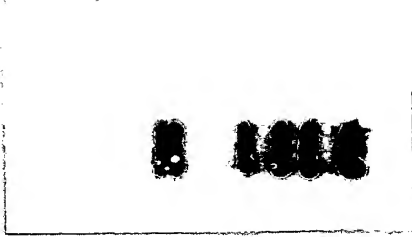
R G G N A G G G Q P G W M L K C K G W E T D A D S Y V Y F T I A A N M 864
 CGTGGTGGTAACGCAGGTGGCGGGCCAGCCAGGCTGGATGCTGAAATGTAAAGGTGGGAAACCGATGGGACTCCCTACGTTTACCTTACCAATCGCTGCAAAACATG 972
 W P Q I C D M I D K P E W K D D P A Y N T F E G R V D K L M D I F S F I
 TGGCCACAGATCTGCGACATGATCGACAAGCCAGAATGGAAAGACGACCCAGCCTACAAACACATTCGAAGGTCGTGTGACAAGCTGATGGACAATCTTCCTTCATC 972
 E T K F A D K D K F E V T E W A A Q Y G I P C G P V M S M K E L A H D P 1080
 GAAACCAAGTTCGCTGACAAGGACAAATTCGAAGTTACCGAATGGGCTGCCAGTACGGCATTCCTTGGGGTCCGGTCAATGTCCATGAAAGAACATGGCTCAGCATCCT
 S L Q K V G T V V E V V D E I R G N H L T V G A P F K F S G F Q P E I T 1188
 TCCCTGCAGAAAGTTGGTACCGTCTGGAAGTTGTCGACGAAATTCGTGGTAACCCACCTGACCGTTGGCGCACCGTTCAAATTCCTCGGATTCAGCCGGAATTACC
 R A P L L G E H T D E V L K E L G L D D A K I K E L H A K Q V V ter 1284 1296
 CGTGCTCGGCTGTTGGGCGAACATACCGACGAAGTTCTGAAAGAACTGGGTCTTGACCGATGCCAAGATCAAGGAACTGCATGCCAAACAGGTAGTTTGATCCGTCAGA
 1311 1323
 CTTTCTGGGCAAAACCGGCACICICCGGAGTCCGTTTITIGTACACAGAAACCCCTAATCAAAACAGCAGTGCATGATTCACATCATTTGCGGCCACATTCATCCT 1404
 TCGGGTCATTACTG.....

-180
ATTGTGTTAAATGACCIGAAATCAATATTGCCGGATTGATCTAGGTCAAATGAATGCAAAATGACITTAIGTCAATGGTGCCAAATGACCTIAGGTCACCGG
-172
-139
-124
-100
-91
-81
-51
-32
-14
1
M S N D D N V
-80
GATTTTTAAAGGGTATGCGGCATACICGGAATTGACGTTAAACAACGTTTAAACAACCAAGGTTTAACTCAIGAGTAACGACGACAATGT
120
E L T D G F H V L I D A L K M N D I D T M Y G V V G I P I T N L A
AGAGTTGACGTGATGGCTTTCATGTTTIGATCGATGCCCTGAAAAATGAATGACATCGATACCATGTATGGTGTTCGGCATTCCTCAATCAGCAACCTGGCT
121
R M W Q D D G Q R F Y S F R H E Q H A G Y A A S I A G Y I E G K P
CGTATGTGGCAAGATGACGGTCAGCGTTTTACAGCTTCGGTCACGAACAACACGCGAGTTATGCAGCTTCTATCGCCGGTTACATCGAAGGAAACCTG
320
G V C L T V S A P G F L N G V T S L A H A T T N C F P M I L L S G S
GCGTTTGCTTGACCGTTTCGCCCTTCCCTGTAACGGCGTGACTTCCCTGGCTCATGCAACCACCACTGCTTCCCAATGATCCGTGTGAGCGGTTT
420
S E R E I V D L Q Q G D Y E E M D Q M N V A R P H C K A S F R I N
CAGTGAACGTGAAATCGTCGATTTCCAAGACGGCGATTACGAAGAAATGGATCAGATGAATGTTCAGCTCCACACTGCAAAAGCTTCTTCCGTATCAAC
520
S I K D I P I G I A R A V R T A V S G R P G G V Y V D L P A K L F
AGCATCAAAGACATTCCAATCGGTATCGCTCGTGACGTTTCGACCCGCTGATCCGGACGTCCAGGTGGTGTTCAGTTGACTTCCAGCAAACTGTTG
620
G Q T I S V E E A N K L L F K P I D P A P A Q I P A E D A I A R A A
GTCAGACCATTTCTGTAGAAGAAGCTAACAACTGCTCTTCAAACCAATCGATCCAGCTCCGGCACAGATTCTTGCTGAAGACGCTATCGCTCGCGCTG
720
D L I K N A K R P V I M L G K G A A Y A Q C D D E I R A L V E E T
TGACCTGATCAAGAAGCCCAACGTCACGTTATCATGCTGGGTAAAGGCGCTGATACGCACAATGCGACGACGAAATCCGGCACCTGGTTGAAGAAACC
820
G I P F L P M G M A K G L L P D N H P Q S A A A T R A F A L A Q C
GGCATCCCATTCCTGCCAATGGGTATGGCTAAAGGCGCTGCTGCTGACAACCATCCACAATCCGCTGCTGCAACCCGCTTTCGCACCTGGCACAGTGTG
920
D V C V L I G A R L N W L M Q H G K T W G D E L K K Y V Q I D I
ACGTTTGCGTACTGATCGGCGCTCGTCTGAACCTGGCTGATGCAGCACCGGTAAAGGCAAAACCTTGGGCGGACGAACTGAAGAAATACGTTTCAGATCGACAT

FIG. 3B

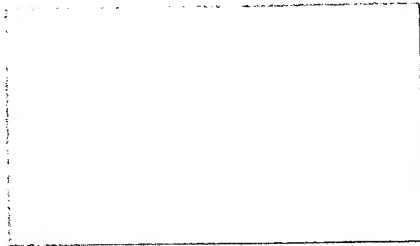
921 Q A N E M D S N Q P I A A P V V G D I K S A V S L L R K A L K G A 1020
 CCAGGCTAACGAAATGGACAGCAACCAGCCTATCGCTGCACCAAGTTGTTGGTGACATCAAGTCCGCCGTTTCCCTGCTCCGCAAGCACTGAAAGGCGCT 1120
 1021 P K A D A E W T G A L K A K V D G N K A K L A G K M T A E T P S G
 CCAAAGCTGACGCTGAATGGACCGGCTCTGAAAGCCAAAGTTGACGGCAACAAGCCAAAGTGGCTGGCAAGATGACTGCCGAAACCCCATCCGGAA 1220
 1121 M M N Y S N S L G V V R D F M L A N P D I S L V N E G A N A L D N T
 TGATGAACCTACTCCAATTCCTGGCGTTGTTGCTGACTTCATGCTGGCAAAATCCGGATATTTCCCTGGTTAACGAAGGCGCTAATGCACTCGACAACAC 1320
 1221 R M I V D M L K P R K R L D S G T W G V M G I G M G Y C V A A A A
 TCGTATGATTGTTGACATGCTGAAACCAACGCTCTTGACTCCGGTACCTGGGTGTTATGGTATGGGTACTGCGTTGCTGCAGCTGCT 1420
 1321 [-----TPP Binding Motif-----]
 V T G K P V I A V E G D S A F G F S G M E L E T I C R Y N L P V T
 GTTACCGGCAACCGGTTATCGCTGTTGAAGGCGATAGCGCATTCGGTTTCTCCGGTATGGAACCTGGAACCATCTGCCGTTACAACCTGCCAGTTACCG 1520
 1421 -----J
 V I I M N N G G I Y K G N E A D P Q P G V I S C T R L T R G R Y D M
 TTATCATCATGAACAATGGTGTATCTATAAAGGTAACGAAGCAGATCCACAACCAAGCGGTTATCTCTGTACCCGCTGACCCGTTGGTTCGTTACGACAT 1620
 1521 M M E A F G G K G Y V A N T P A E L K A A L E E A V A S G K P C L
 GATGATGGAAGCATTTGGCGGTAAAGTTATGTTGCCAATACTCCAGCAGAACTGAAAGCTGCTCTGGAAGAAGCTGTTGCTTCGGGCAAAACCATGCCTG 1720
 1621 I N A M I D P D A G V G S G R I K S L N V V S K V G K K 1705
 ATCAACGCGATGATCGATCCAGACGCTGGTGTGCAATCTGGCCGTATCAAGAGCCTGAACGTTGTAAGTAAAGTTGGCAAGAAATAATTAGCCCAACTTT 1820
 1721 1758
 GATGACCGGTTACGACCGGTCACATAAAGTGTTTCGAAIGCCCTICAAGTTTACTIGAAGGGCATTTTTTACCTTGCAGTTTATAAACAGGAAAAATTGT 1908
 1821 ATTACAGCGGAAAGCAGATTAAAGCCAGAGAAACATTTCTTTTTATTGAAAATTGCCATAAACACATTTTTTAAAGCTGGCTTTT

AP 15
MW markers



23,130 bp
6,557 bp
2,322 bp

AP 34
MW markers



23,130 bp
6,557 bp
2,322 bp

AP 273
MW markers



23,130 bp
6,557 bp
2,322 bp

FIG. 4

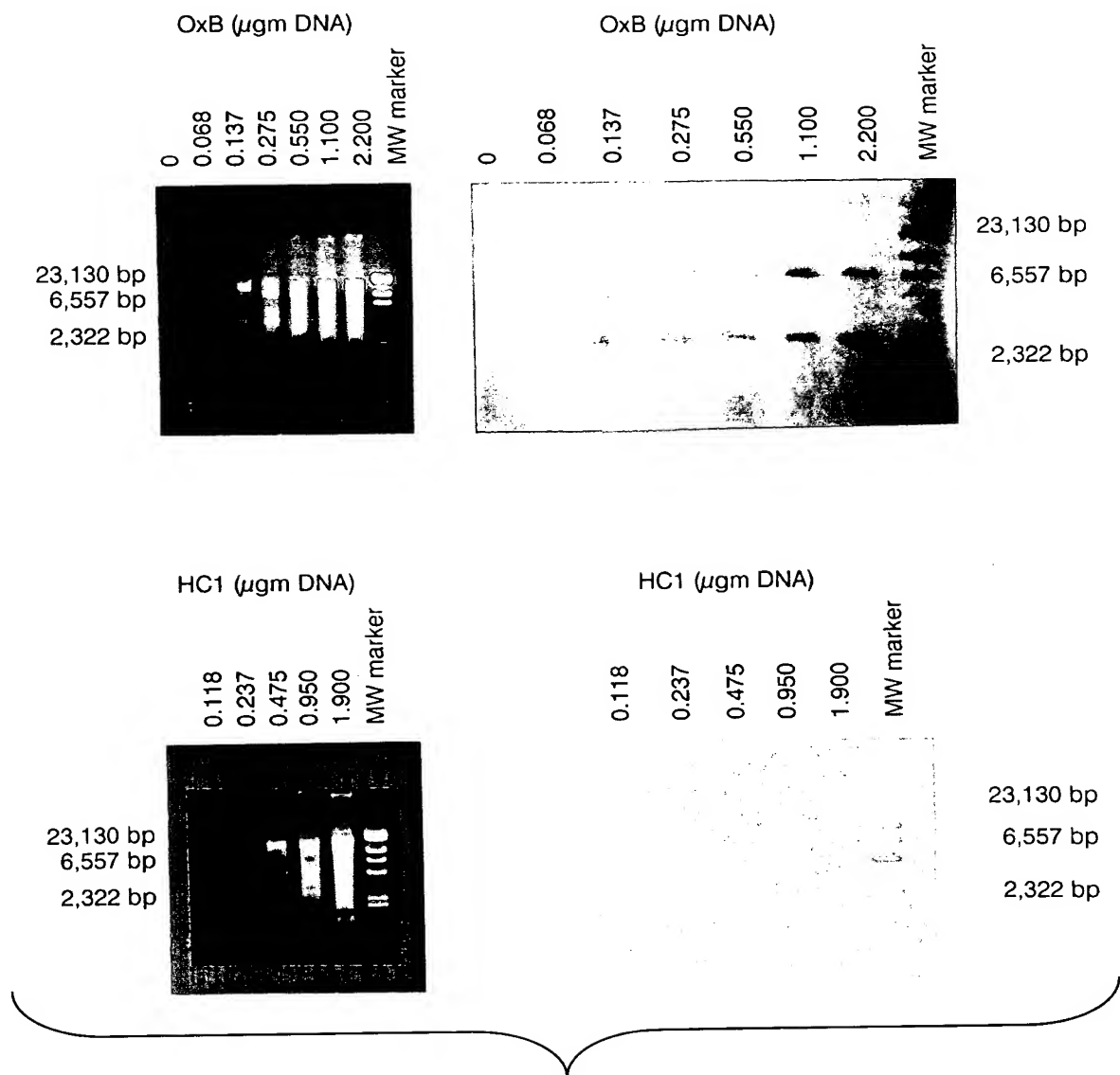


FIG. 5

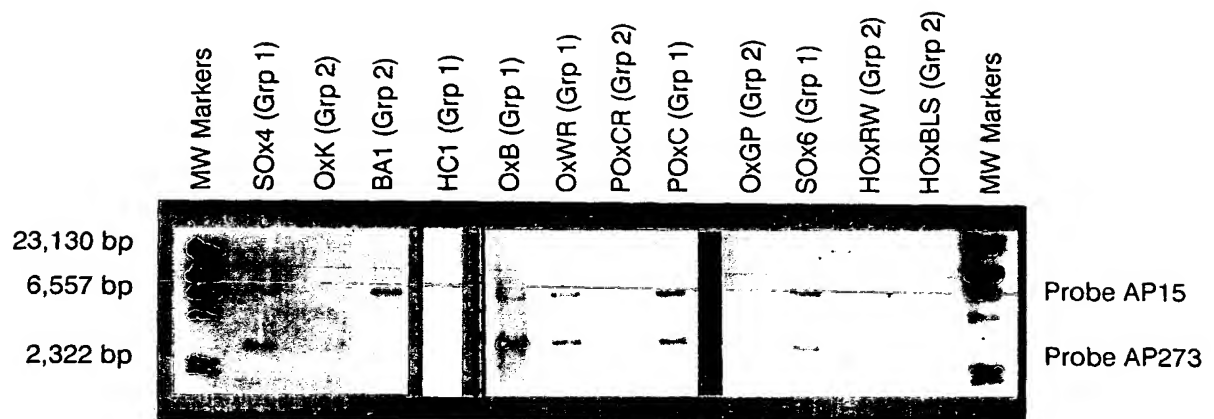


FIG. 6

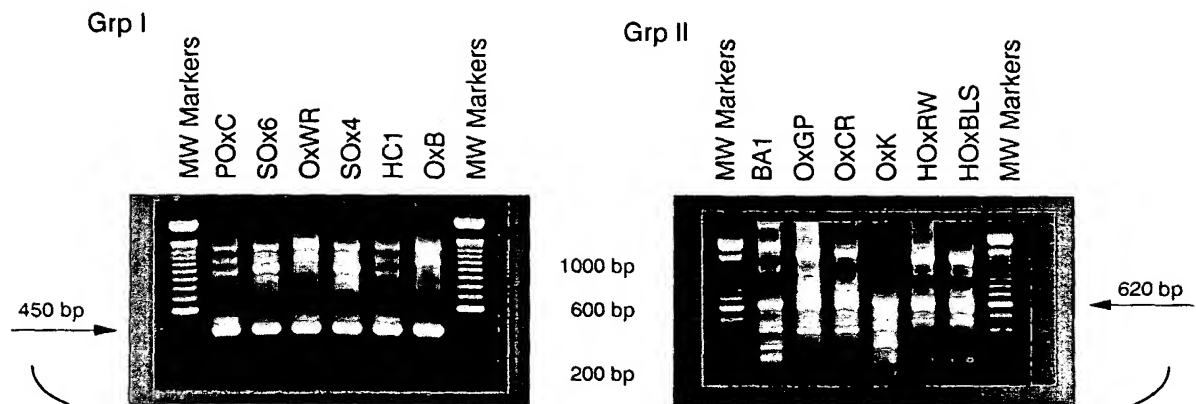


FIG. 7

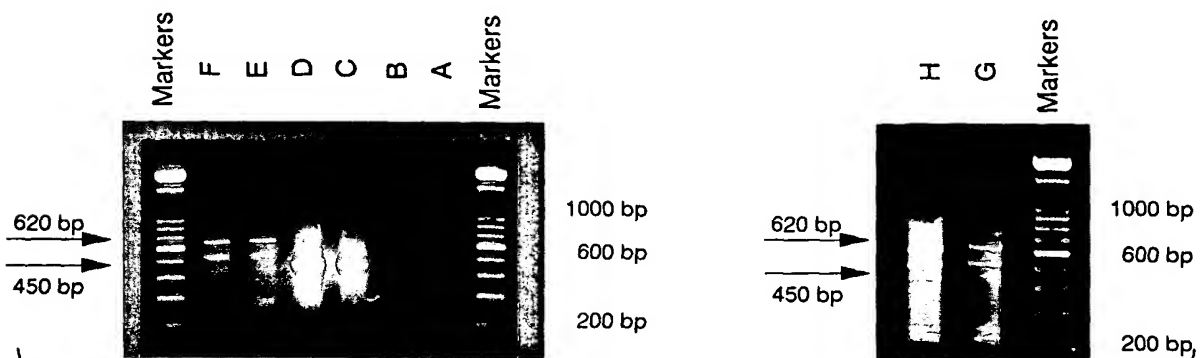


FIG. 8

FIG. 9A

[illegible]

115	(AP307)	192
L A R M W Q D D G Q R F Y S F R H E Q H A G Y A A S		
OxBCTGGCTCGTATGTGGCAAGATGACGGTCAGCGTTTTACAGCTTCCGTACGGAACAACAGCAGGTTATGCAGCTTCT	
	↓	
HClCTGGCTCGTATGTGGCAAGATGACGGTCAGCATTTTACAGCTTCCGTACGGAACAACAGCAGGTTATGCAGCTTCT	
	↓	
gpICTGGCTCGTATGTGGCAAGATGACGGTCAGCGTTTTACAGCTTCCGTACGGAACAACAGCAGGTTATGCAGCTTCT	
CTGGCTCGTATGTGGCAAGATGACGGTCAGCGTTTTACAGCTTCCGTACGGAACAACAGCAGGTTATGCAGCTTCT	
	↓	↓ ↓
	↓	↓ ↓
TTGGCTCGTATGTGGCAAGATGACGGTCAGCGTTTTACAGCTTCCGTCAATGAACAACAGCAGGCTACGCAGCATCT	
TTGGCTCGTATGTGGCAAGATGACGGTCAGCGTTTTACAGCTTCCGTCAATGAACAACAGCAGGCTACGCAGCATCT	
HOxRA		
HOxUK90		

[illegible]

FIG. 10A

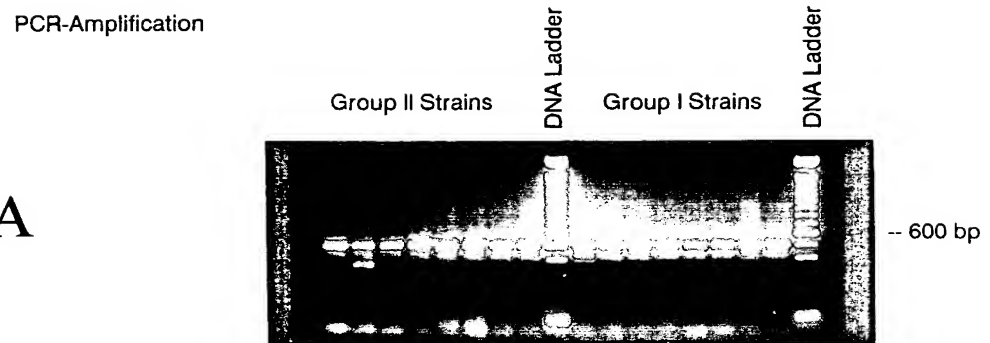
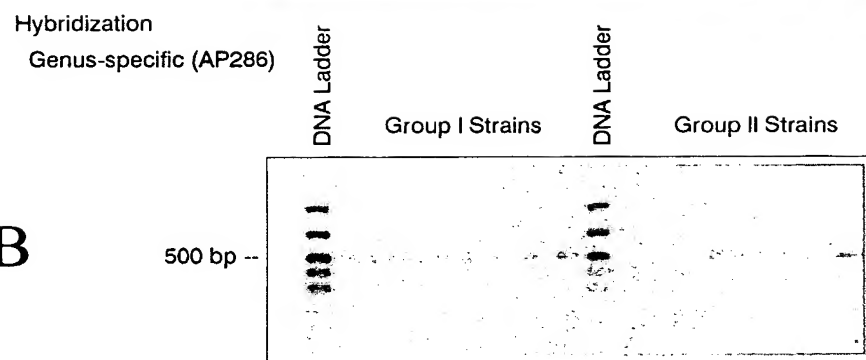
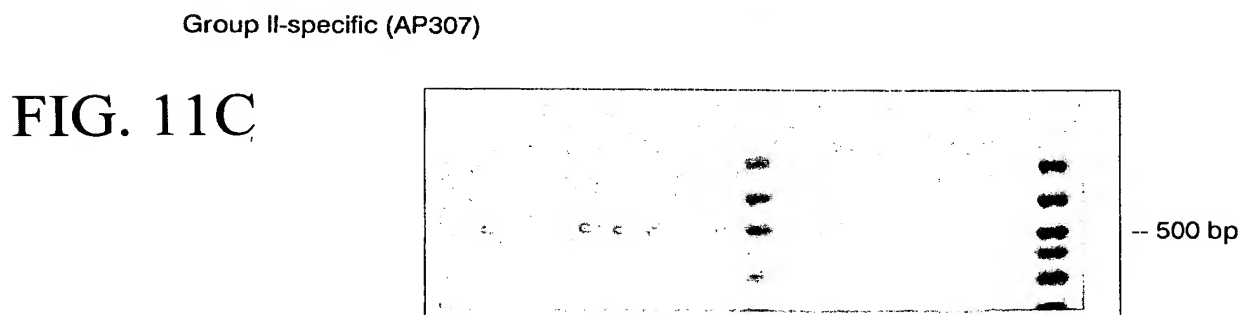
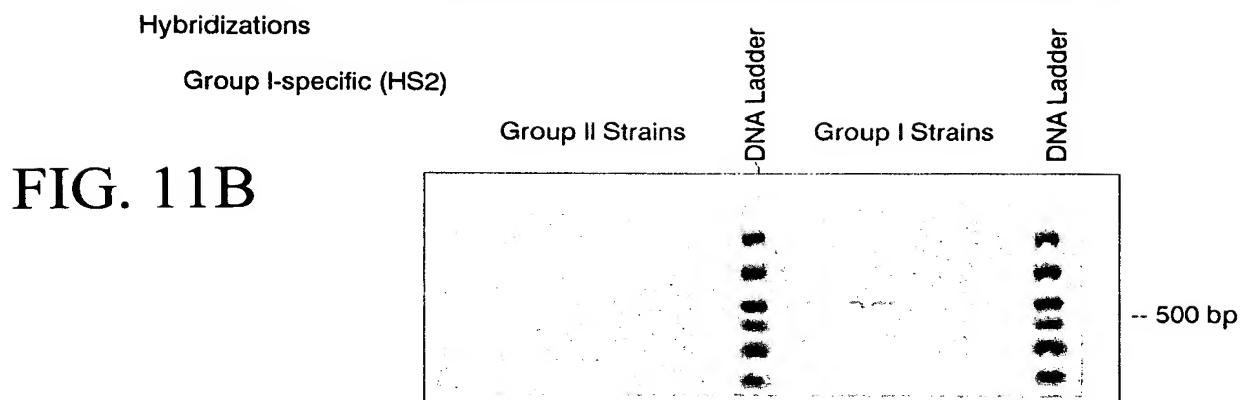
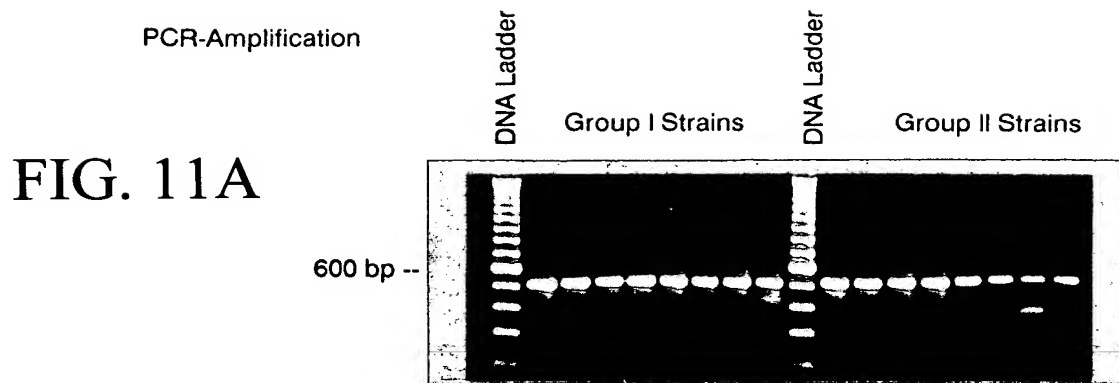


FIG. 10B





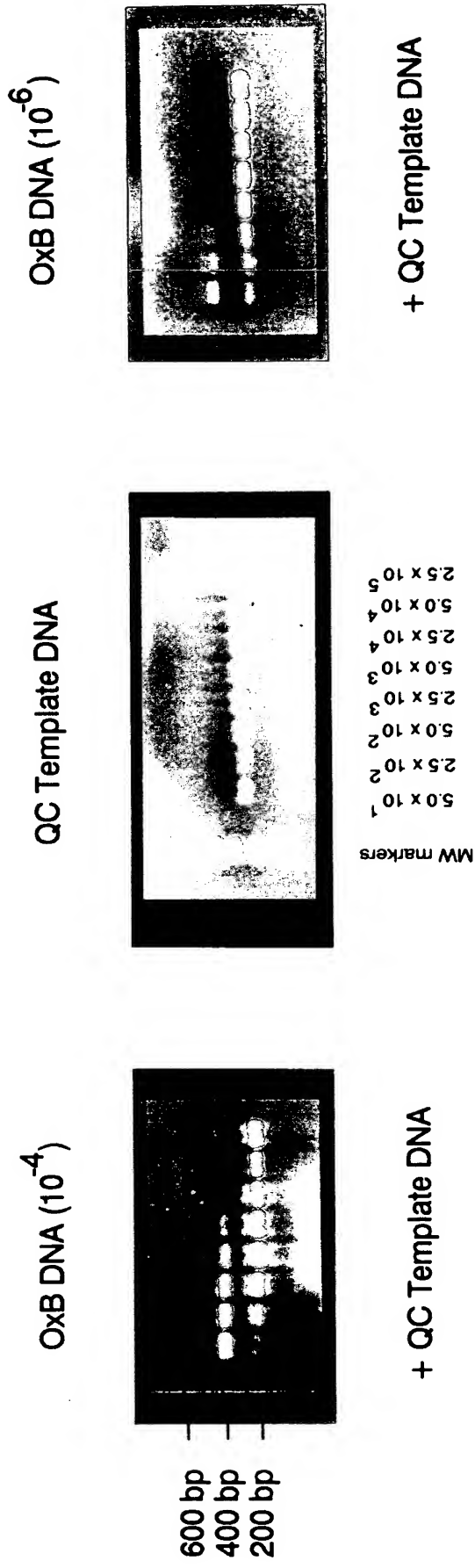


FIG. 12A

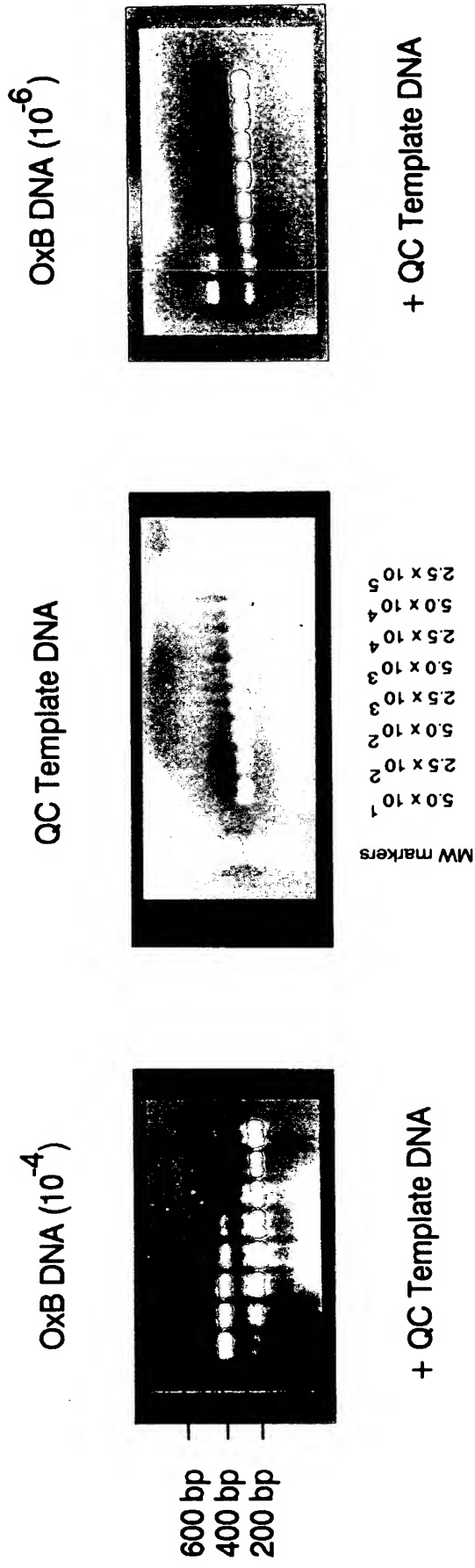


FIG. 12B

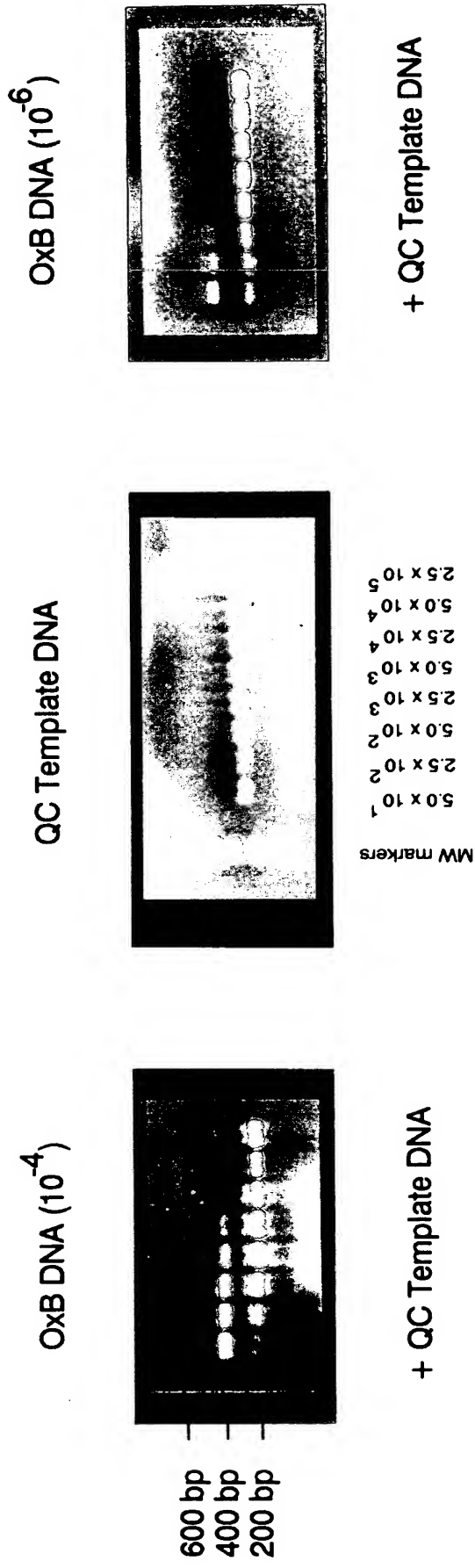
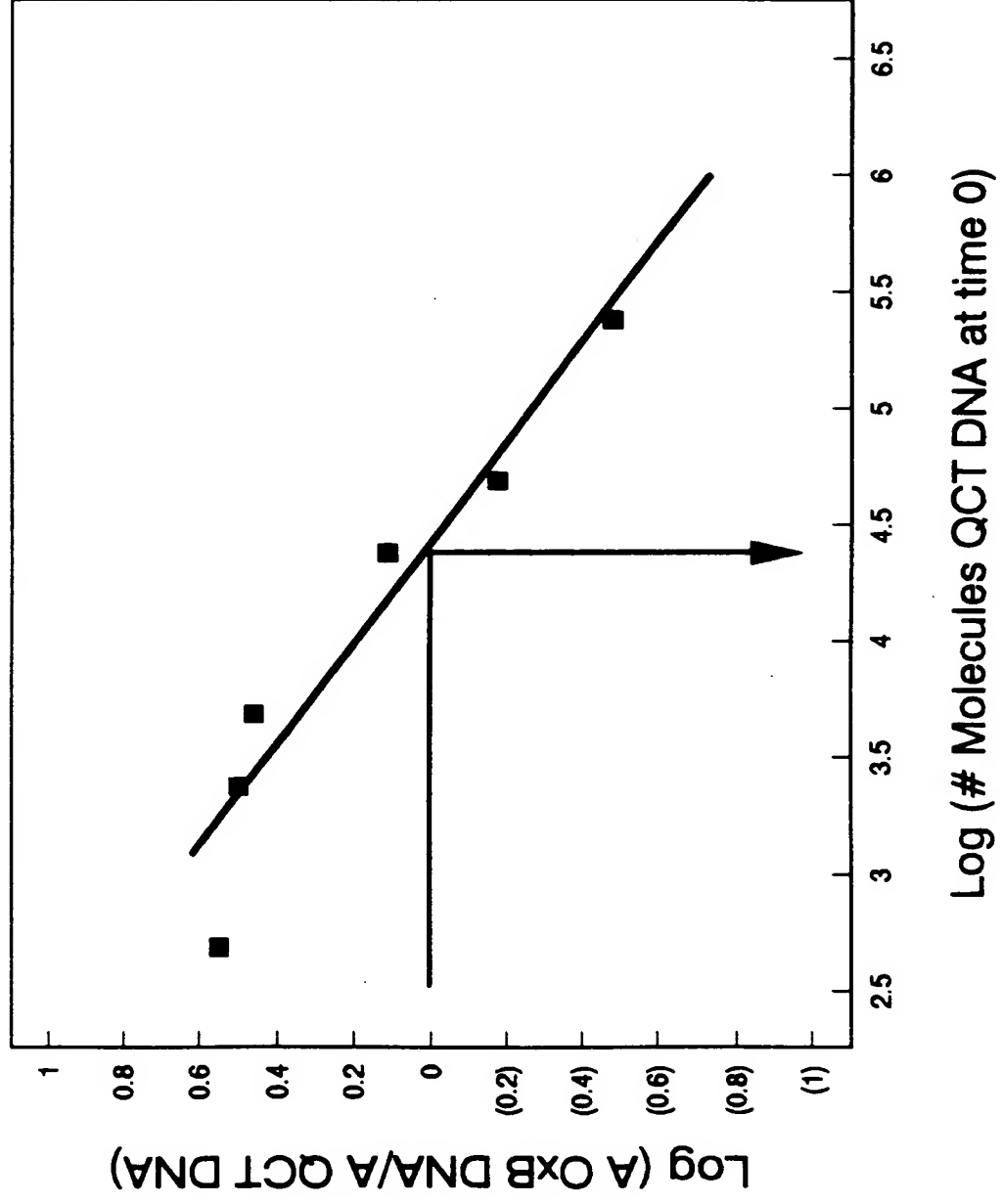


FIG. 12C

FIG. 12D



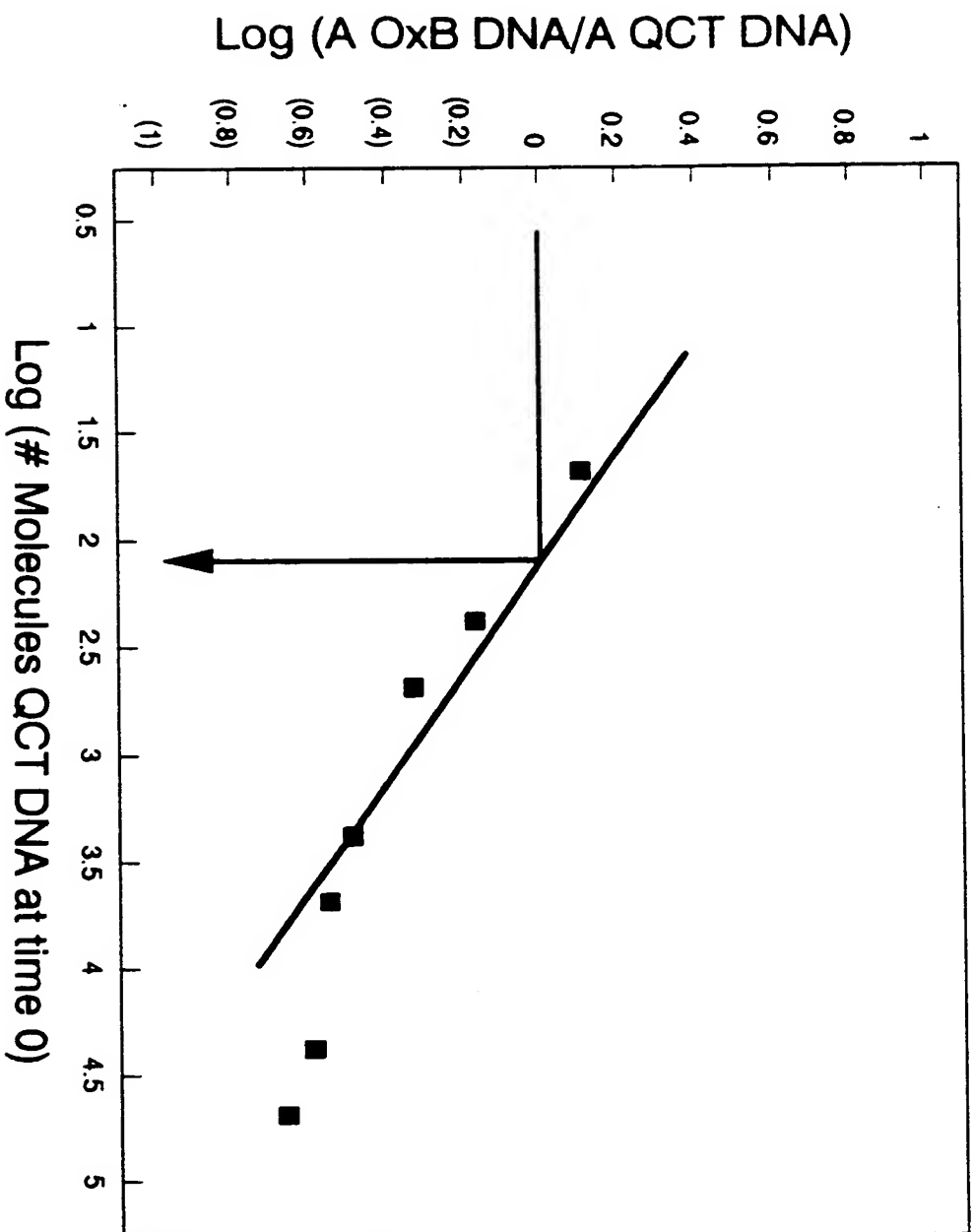


FIG. 12E